

FIGURE 1

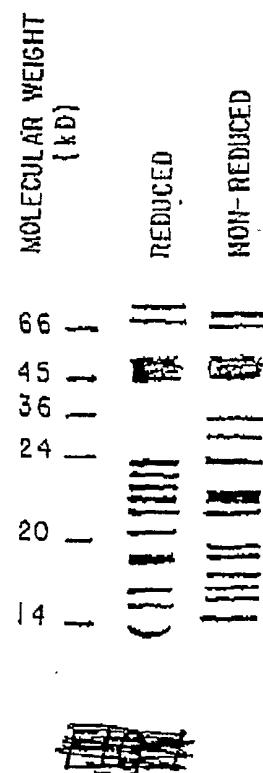


FIGURE ■ 2

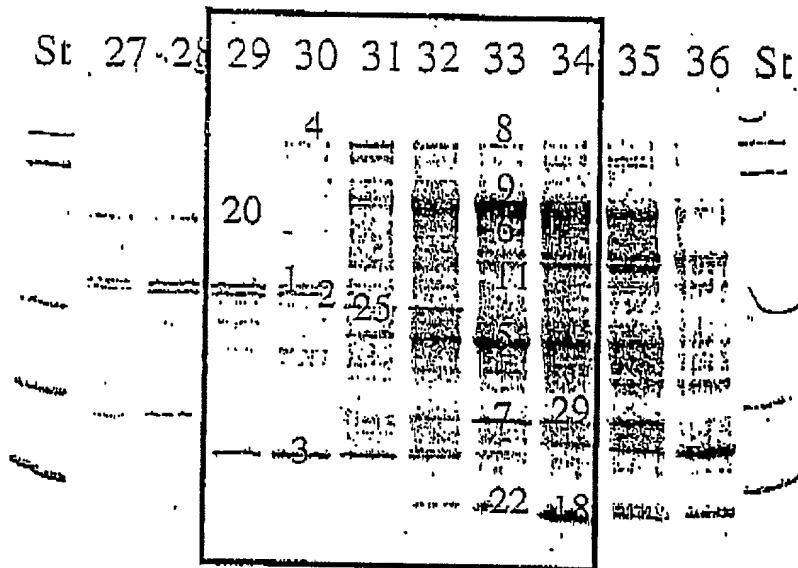
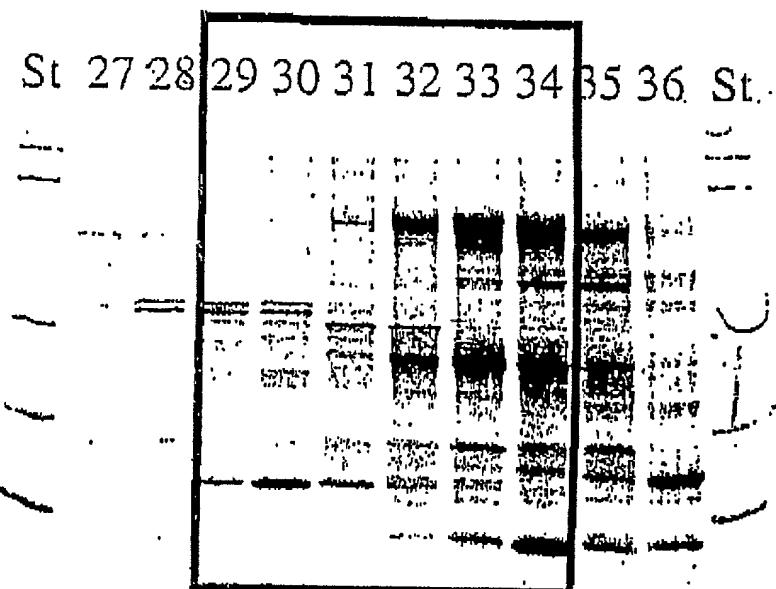
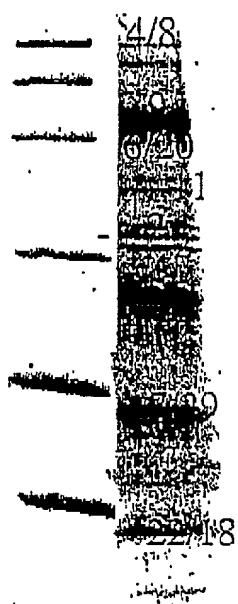


FIGURE ■ 3

St. BP



Band No.	Identity
1	histone H1.c
2	histone H1.c
3	ribosomal protein RS20
4	similar to ribosomal protein LORP
5	BMP-3
6	$\alpha 2$ macroglobulin RAP & BMP-3
7	similar to ribosomal protein LORP
8	BMP-3
9	BMP-3
11	ribosomal protein RL6 & BMP-3
18	TGF- β 2/SPP24
20	Factor H
22	TGF- β 2
25	BMP-3 & H1.x
29	BMP-3 & ribosomal protein RL32

FIGURE 2-4

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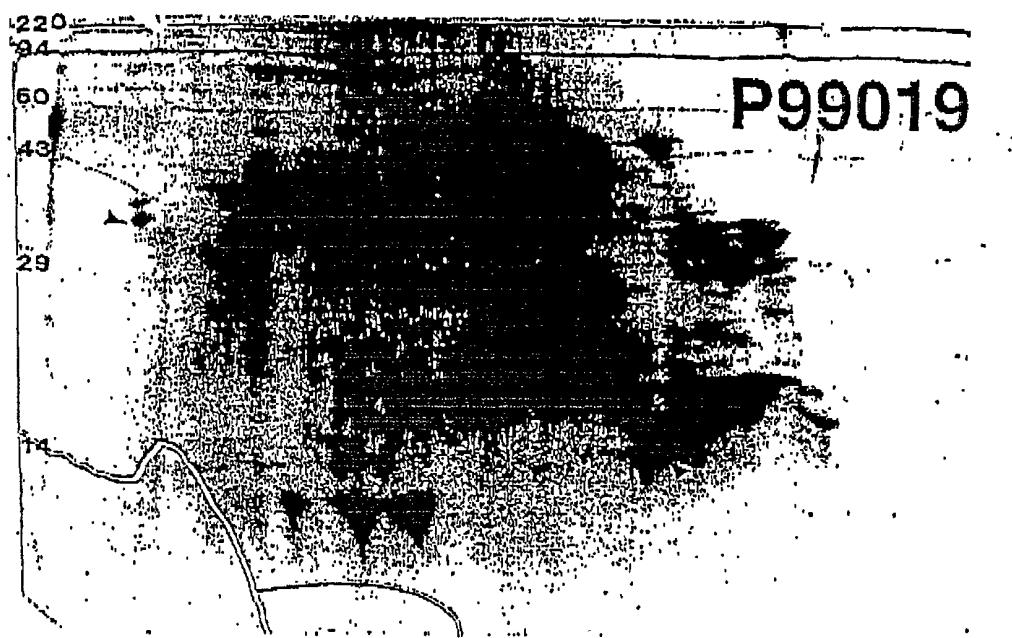


FIGURE 5

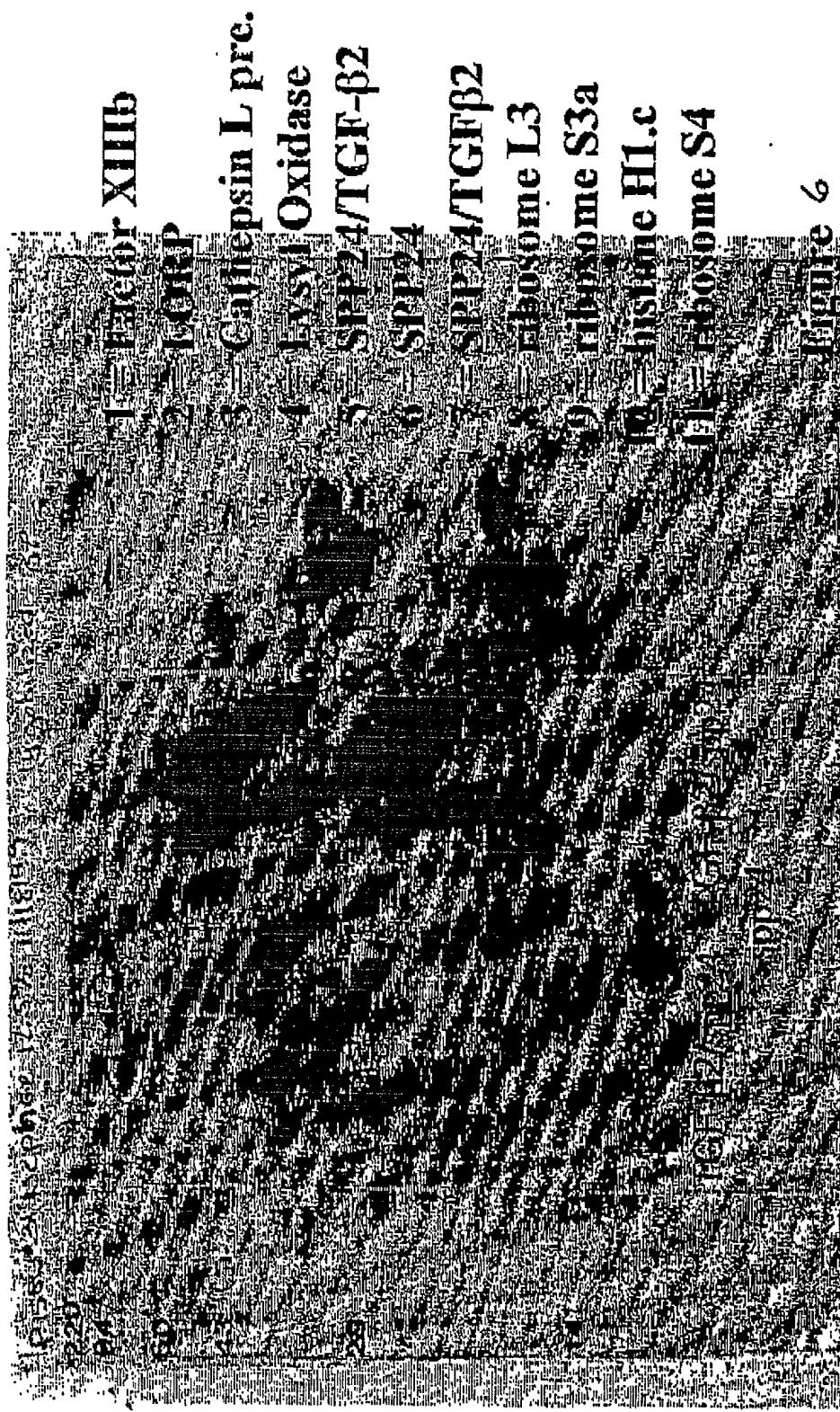


Figure 6

Figure 2A. (Band 1)

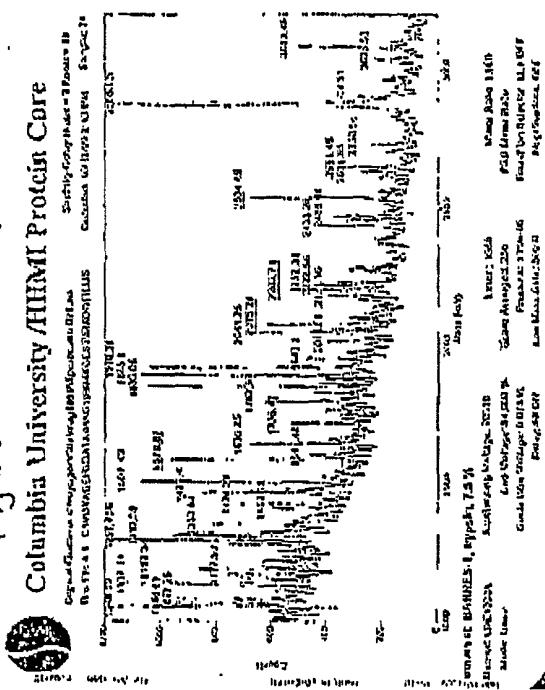
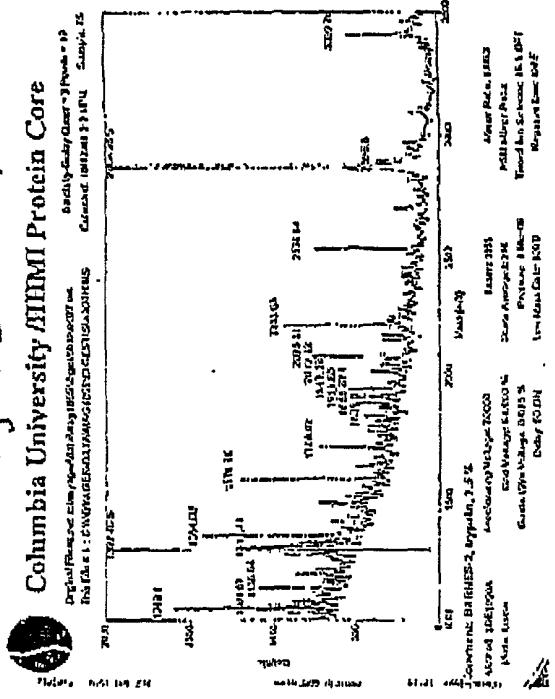
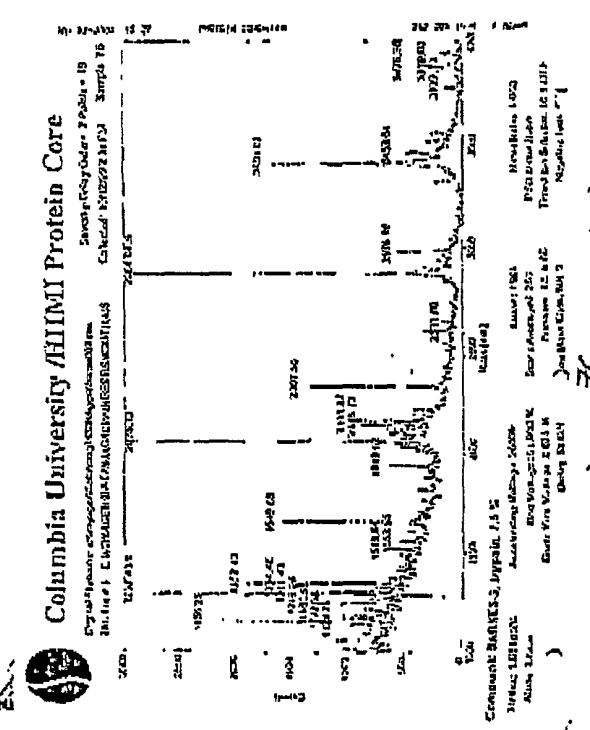


Figure 7B (Band 2)



Columbia University JHUIMI Protein Core



Columbia University / HBCU Protein Core

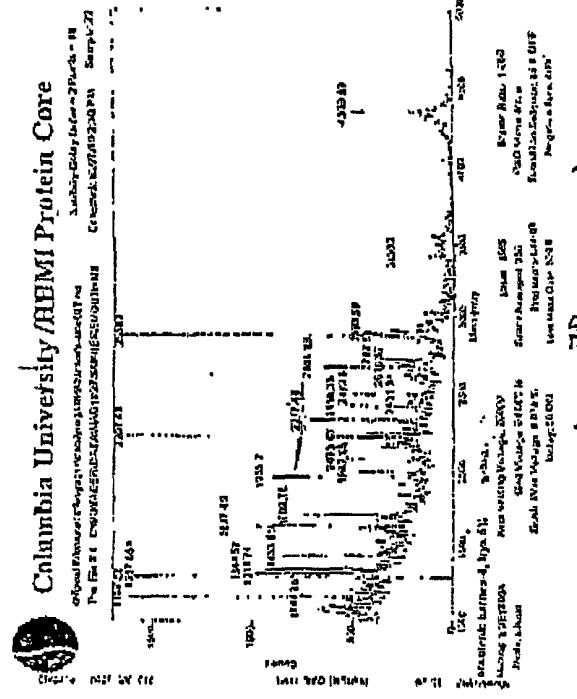
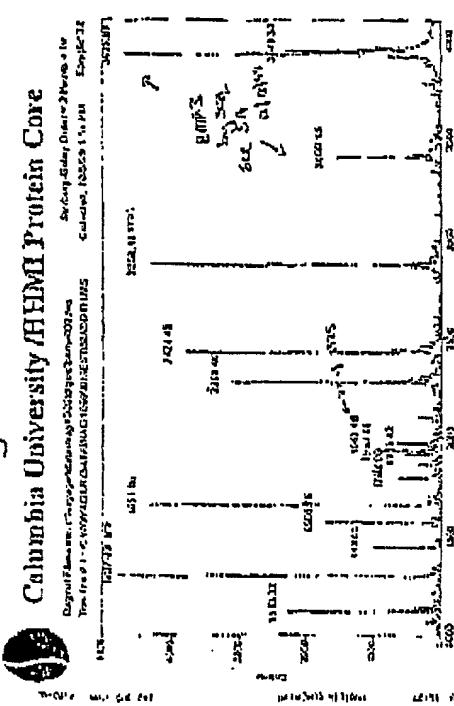


Figure 7D (Band 4)

Figure 7c (Band 3)

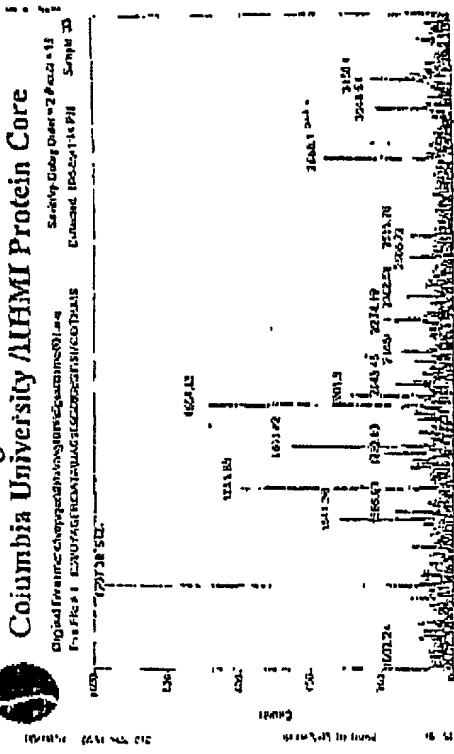
Figure 7E (Band 5)



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Figure 7F (Band 6)



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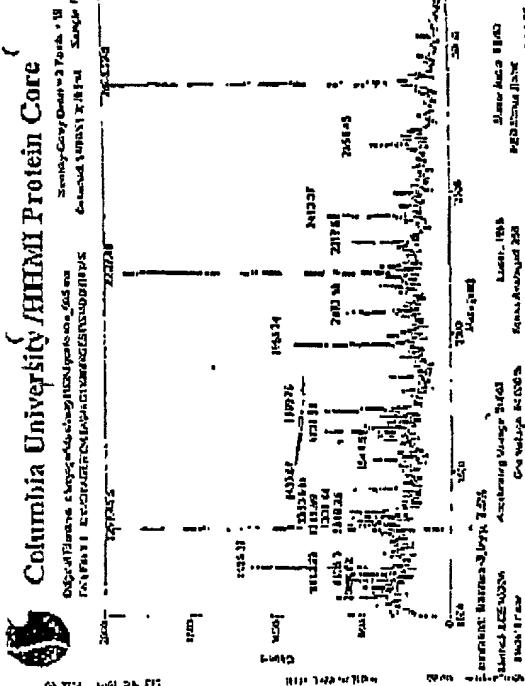


Figure 7G (Band 7)

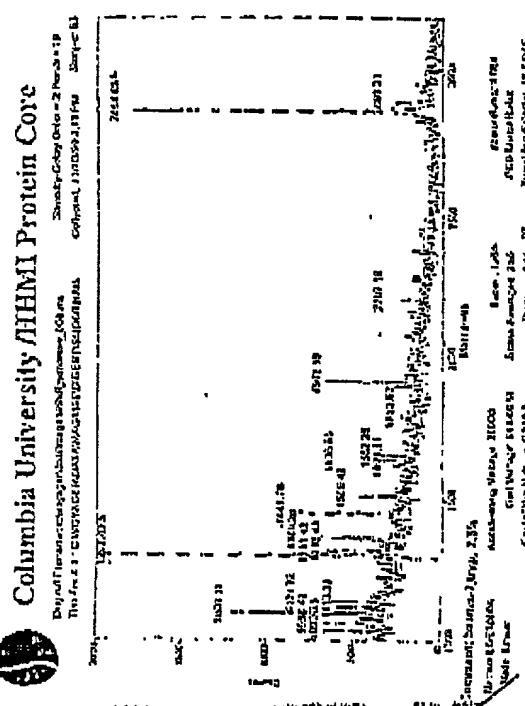


Figure 7H (Band 8)

Figure 7I (cont'd a)

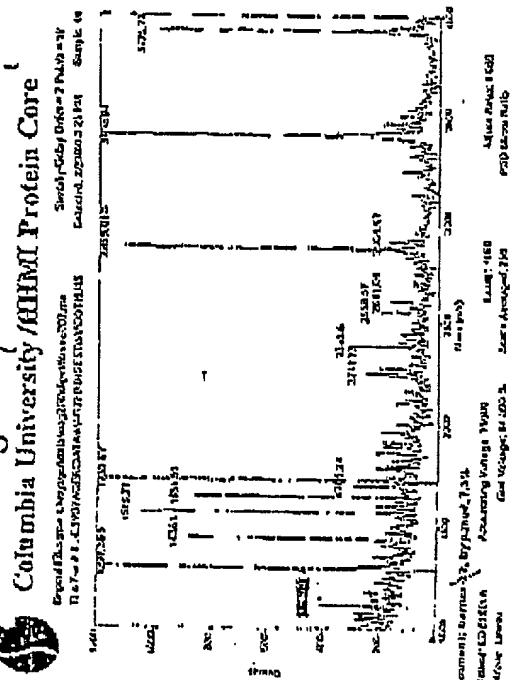
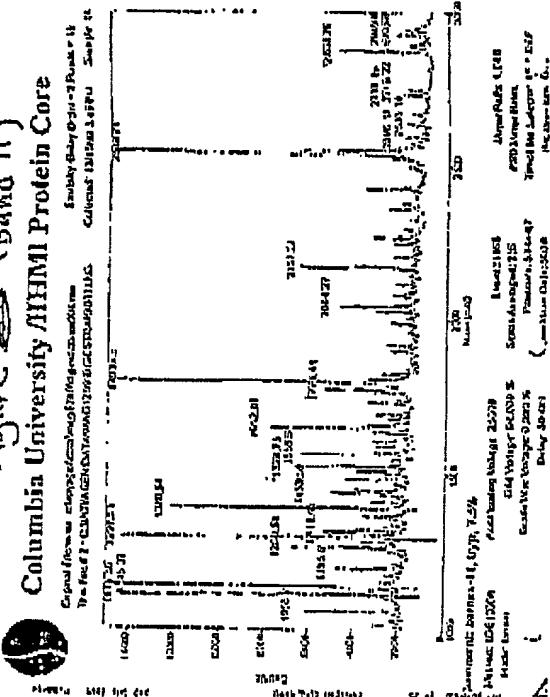
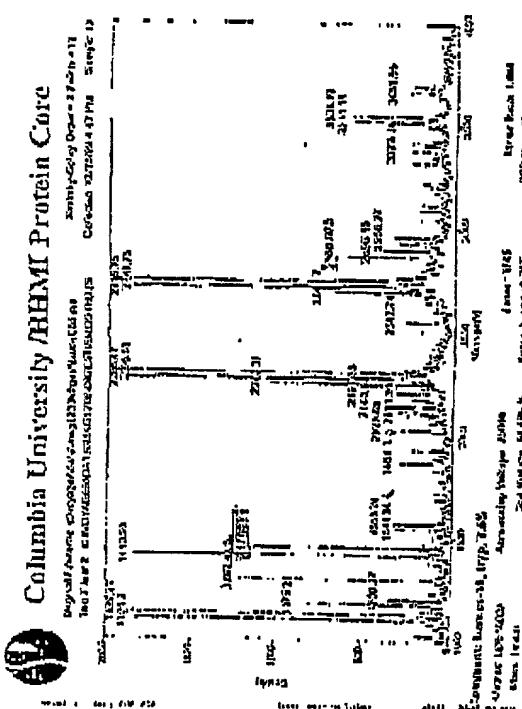


Figure 7.J (Band II)
a University of Miami Protein Core



Columbia University / HHMI Protein Core



Columbia University /HEMI Protein Core

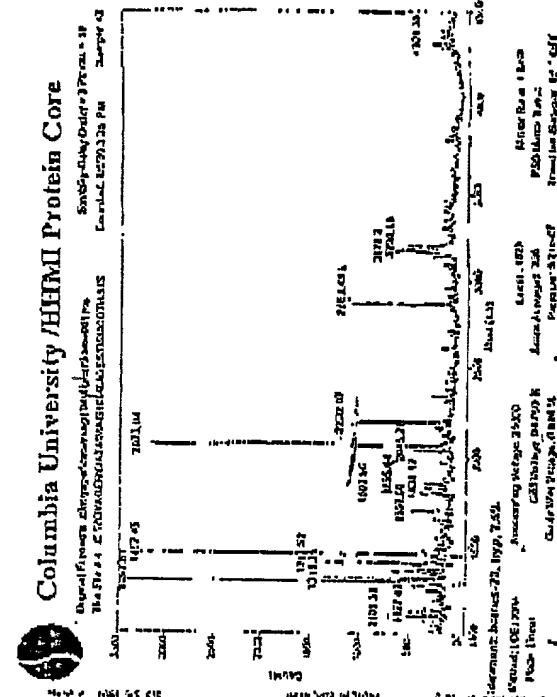


Figure 1 (Panel B)

Figure 2 (Band 20)

Figure ~~TM~~ (Band 22)

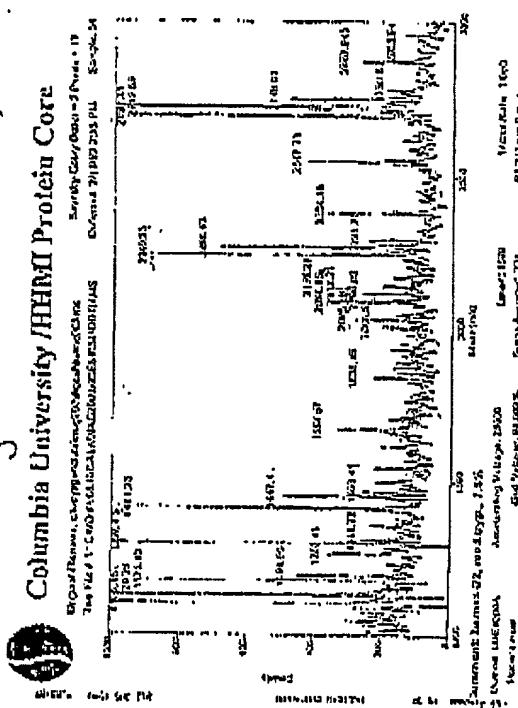


Figure 7N (Band 25)

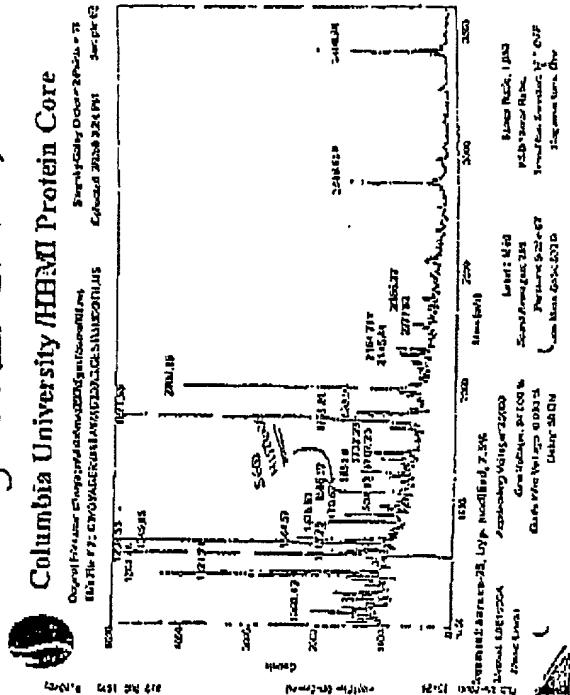


Figure 70 (Band 29)  Impulse is indicated by a vertical tick mark at the right end of the wavelet.

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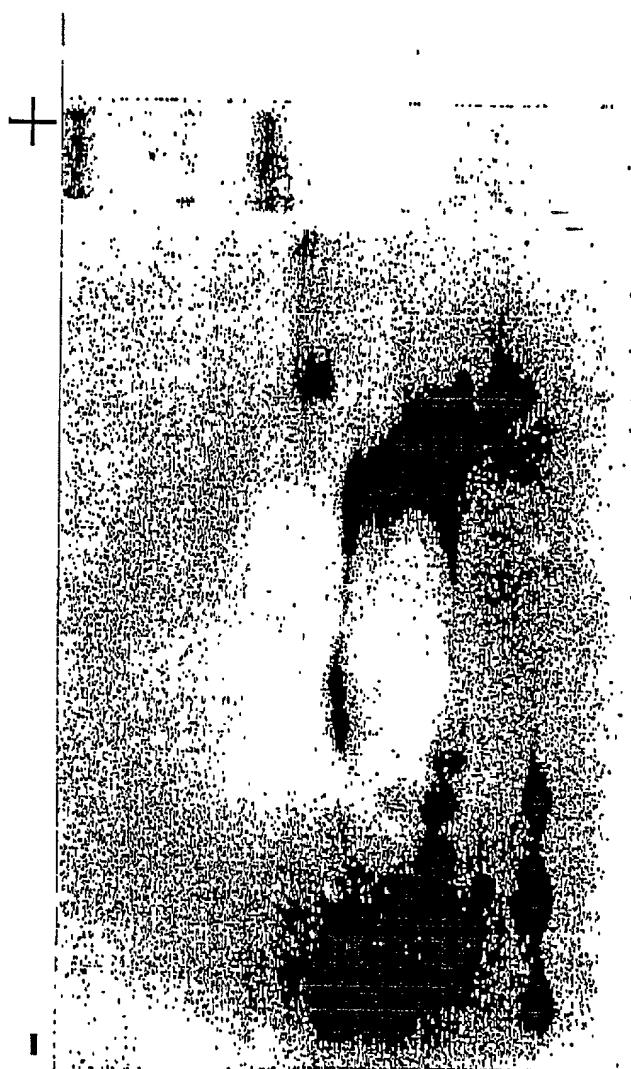


FIGURE 8

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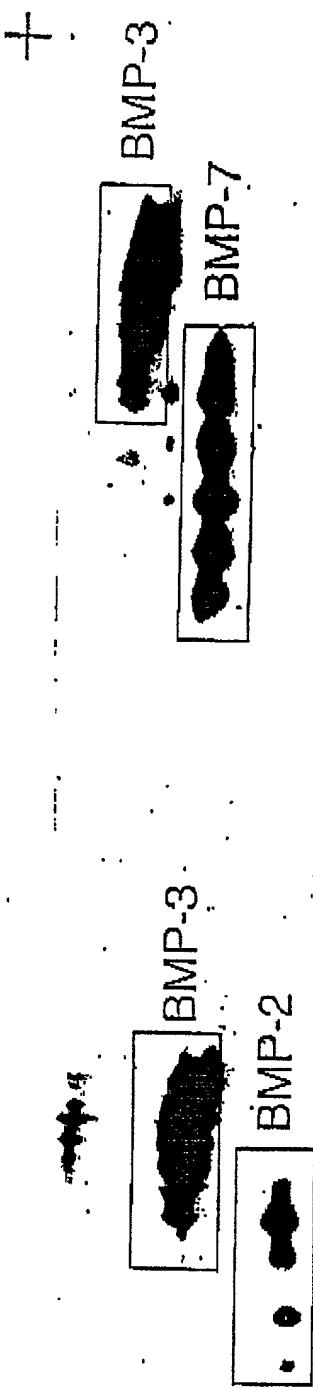


FIGURE 9B



FIGURE 9C

FIGURE 9D

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FIGURE 10

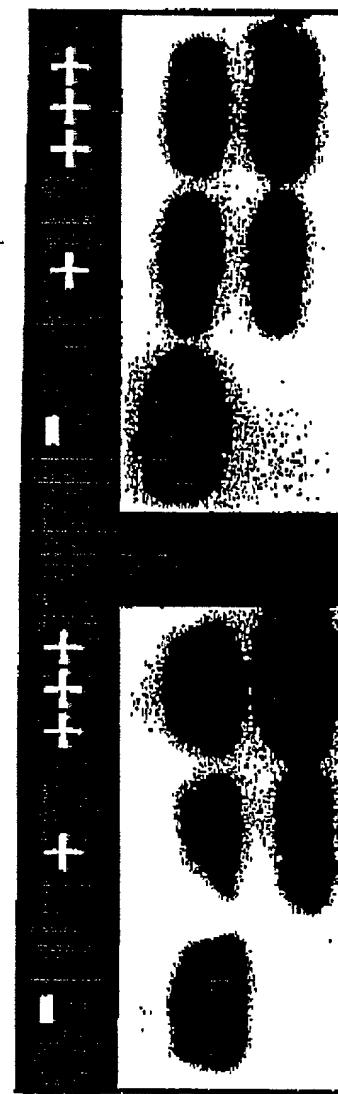
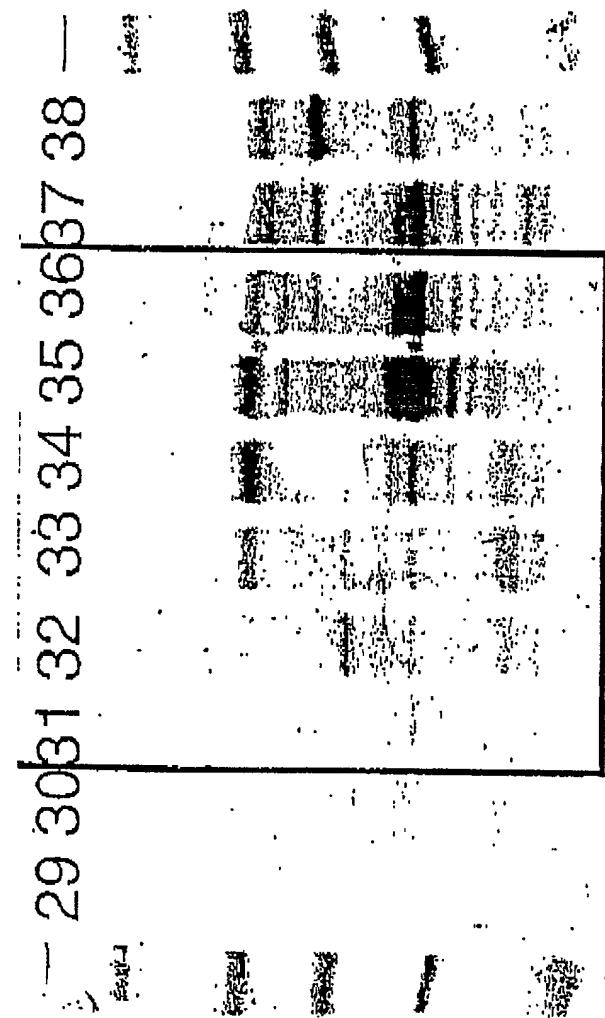


FIGURE 11

FIGURE 12

FIGURE 22 13A

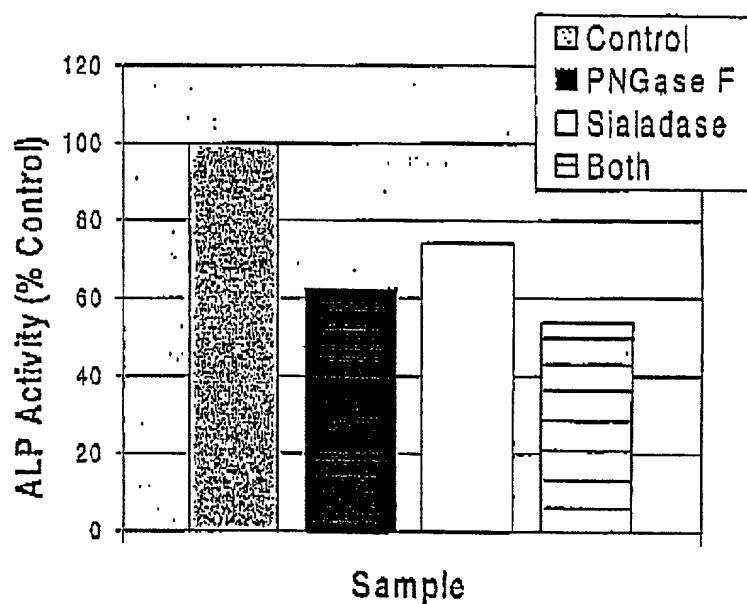
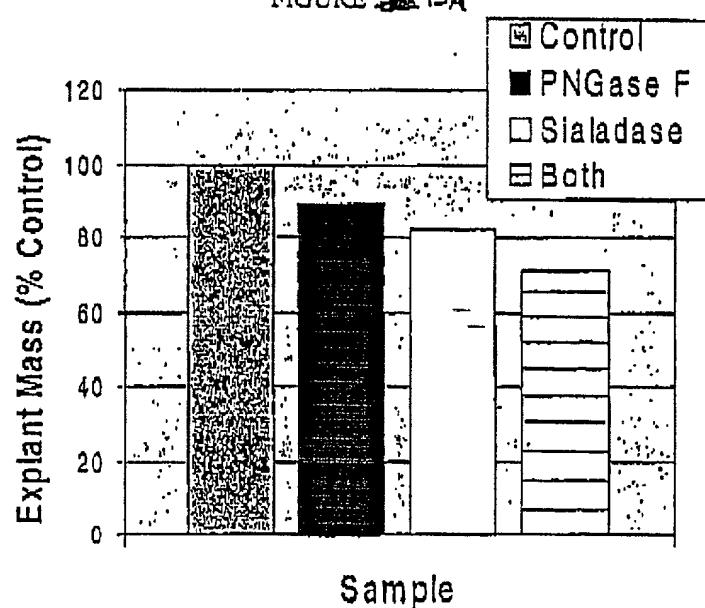


FIGURE 22 13B

Figure 14 Antibody Listing

Specificity	Antigen	Host Species	PCM/C	Source	Catalog No.
TGF- β 1 (human)	Protein	Rabbit	Polyclonal	Prontega	G1221
TGF- β 2 (human)	Peptide	Rabbit	Polyclonal	Santa Cruz Biotechnology	sc-90
TGF- β 3 (human)	Peptide	Rabbit	Polyclonal	Santa Cruz Biotechnology	sc-82
BMP-2 (human)	Protein	Rabbit	Polyclonal	Austral Biologics	PA-513-9
BMP-3 (human)	Peptide	Chicken	Polyclonal	Research Genetics	NA
BMP-4 (human)	Peptide	Goat	Polyclonal	Santa Cruz Biotechnology	sc-6896
BMP-5 (human)	Peptide	Goat	Polyclonal	Santa Cruz Biotechnology	sc-7405
BMP-6 (human)	Peptide	Mouse	Monoclonal	Novocastra Laboratories	NCL-BMP6
BMP-7 (human)	Peptide	Rabbit	Polyclonal	Research Genetics	NA
TGF- β 1 (human)	Peptide	Goat	Polyclonal	Santa Cruz Biotechnology	sc-1884
osteonectin (bovine)	Protein	Mouse	Monoclonal	DSTIB	AON-1
osseocalcin (bovine)	Protein	Rabbit	Polyclonal	Accurate Chemicals	A761/R11
serum albumin (bovine)	Protein	Rabbit	Polyclonal	Chemicon International	AB870
transferin (human)	Protein	Chicken	Polyclonal	Chemicon International	AB797
apo-A1 lipoprotein (human)	Protein	Goat	Polyclonal	Chemicon International	AB740

Figure 15A Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments from 1D Gels

Band	Sample	Sequence Data	Best Database Match	Match Identification	Species	Acc. No.	Ref
1							
2	Ix 49 (1579)	XLAAGGYDVEK	ALAAAGGYDVEK	11/11 histone H1.c	human	675668 (NCBI)	65-75
3	Ix 67 (1346)	SLEKVCADLIR	SLEKVCADLIR	11/11 40s Ribosomal Protein S20	rat	R3RT2D (PIR)	31-41
4	Ix 65 0	(Y)VCGMLGFPSEARV	WCGMLGFPGEKRV	11/14 LORP	mouse	AAC953311 (NCBI)	213-228
5	N-terminal seq	STGVLLPQNNELPG	STGVLLPQNNELPG	15/15 BMP-3	human	4557371 (NCBI)	290-304
6x 72 (3825)	STGVLLPQNNELPGA EYQY	STGVLLPQNNELPGA AEYQY	20/20 BMP-3	human	4557371 (NCBI)	290-309	
6x 74 (3409)	STGVLLP1Q	STGVLLP1Q	9/9 BMP-3	human	4557371 (NCBI)	290-298	
6	Ix 55 (1586)	(S)QTLOFRE	SQTLOFDE	7/6 BMP-3	human	4557371 (NCBI)	346-353
Ix 47	WYAF	no match		7/7			
N-terminal seq	HAGKYSREKNTV(P)AP)	[HAGKYSREKNTV(P)AP]	11/14 α -2-Macroglobulin Receptor Assoc. Pro.	human	P3053 (Swiss-Prot)	31-46	
Ix 57 (1438)	SQTLQFDEQ	SQTLQFDEQ	9/9 BMP-3	human	4557371 (NCBI)	346-354	
Ix 57 (1852)	SLKPSNHA	SLKPSNHA	8/8 BMP-3	human	4557371 (NCBI)	410-417	
Ix 51 (1093)	AALRPLVCP	AALRPLVCP	9/9 60s Ribosomal Protein L32	mouse	P17832 (Swiss-Prot)	1-8	
Ix 37 (no MS)	A(I)(Q)VERYV	AVER	5/5 60s Ribosomal Protein L32	mouse	P17832 (Swiss-Prot)	10B-113	
Ix 37 (no MS)	A(I)(Q)VERYV	HQSDRYV	5/7 60s Ribosomal Protein L32	mouse	P17832 (Swiss-Prot)	22-23	
Ix 78 0	XALFGIAQLGXALGP	no match	7/7				
Ix 56 (1587)	SQTLQFDEQT	SQTLQFDEQT	10/10 BMP-3	human	P12645 (Swiss-Prot)	346-355	

Figure 15B Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments from 1D Gels

Band Sample	Sequence Data	Best Database Match	Match Identification	Species	Acc. No.	AAs
11 (x 55 (131))	SQTLXLF	SQTLQF	5/6	BMP-3	human (NCBI)	346-351
1x 47 (1772)	MATVTKPVGGDK	VLATVTKPVGGDK	13/13	60s Ribosomal Protein L6	human (Swiss-Prot)	67-93
x 76 (1795)	xMFAL	xMFAL	4/4	60s Ribosomal Protein L6	human (Swiss-Prot)	273-276
x 61 (1145)	AVPQLQGYLR	AVPQLQGYLR	9/10	60s Ribosomal Protein L6	human (Swiss-Prot)	262-271
1B						
22 (x 58 (1101))	ALDAAYCFR	ALDAAYCFR	9/9	TGF-β2	human (Swiss-Prot)	303-311
x 63 (no match)	GYNANFCAGACPYL	GYNANFCAGACPYL	14/14	TGF-β2	human (Swiss-Prot)	340-353
x 66 (1411.71)	VNSQSLSPY	VNSQSLSPY	9/9	SFP24	bovine (Swiss-Prot)	42-50
25 (x 39 (1470))	KAAKPSV(P)	KAAKPSV(P)	8/8	Histone H1.x	human JC4928 (PIR)	199-206
29						

fx = fraction number (molecular weight of fragment, as measured by SDS-PAGE)

Figure 1A Identification of Proteins by Mass Spectrometry of Tryptic Fragments from 1D Gels

Band	Mass Spec Profile	Species	Acc. No.	Mass Spec Data	Mass Spec Database	Mass Difference	AAs	% Coverage	Comments
1	4 peaks match with histone H1.c	human	87668 (NCBI)	1172.97	1172.37	0.60	110-121	22	15 MS peaks match with Band 2
				1579.87	1579.71	0.16	55-78		
				1708.47	1707.89	0.58	64-79		
				2011.58	2012.32	-0.74	35-54		
2	3 peaks match with histone H1.c	human	87668 (NCBI)	1579.76	1579.71	0.05	65-79'	16	Identification of started peptide confirmed by sequence analysis
				1708.02	1707.89	0.13	64-79		
				2012.12	2012.32	-0.20	35-54		
3	7 peaks match with ribosome S20	rat	R3R120 (PIF)	1129.76	1129.40	0.36	50-59	62	15 MS peaks match with Band 1
				1156.21	1156.30	-0.09	76-83		
				1334.46	1334.62	-0.16	58-66		
				1352.13	1351.53	0.59	88-99		
				1518.04	1517.77	0.27	8-21		
				1919.02	1919.19	-0.17	5-21		
				3404.02	3404.87	-0.85	88-119		
4	3 peaks match with Lysyl Oxidase RP	human	NP002309 (Swiss-Pro)	1907.95	1906.27	-0.52	150-167	8	12 MS peaks match with Band 8
				2410.35	2410.63	-0.28	64B-66B		
				2610.57	2610.10	0.47	455-478		

Figure 16B Identification of Proteins by Mass Spectrometry of Tryptic Fragments from 1D Gels

Band	Mass Spec Profile	Species	Acc. No.	Mass Spec Data	Mass Spec Database	Mass Difference	AAs	% Cover-age	Comments
5	9 peaks match with BMP-3	human	4557371 (NCBI)	1113.32	1113.31	0.01	361-368	48	% coverage calculation is relative to the mature BMP-3, 183 AAs (290-472)
			1438.53	1438.50		-0.05	346-357		
			1586.76	1586.76		0.00	345-357		
			1651.86	1651.91		-0.05	410-424		
			1794.09	1794.02		0.07	346-350		
			2268.46	2268.63		-0.17	374-392		
			2424.45	2424.81		-0.36	373-392		
			3409.15	3407.77		1.38	292-318*		
6	3 peaks match with α_2 -Macroglobulin RAP	human	P30533 (Swiss-Pro)	1002.24	1002.15	0.09	283-290	17	
				2362.56	2362.43	0.15	129-150		
			3048.51	3048.52		-0.01	257-282		
	2 peaks match with BMP-3	human	4557371 (NCBI)	1566.93	1566.75	0.18	346-357	15	% coverage calculation is relative to the mature BMP-3, 183 AAs (290-472)
			1651.88	1651.91		-0.03	410-424		

Figure 16C Identification of Proteins by Mass Spectrometry of Tryptic Fragments from 1D Gels

Band	Mass Spec Profile	Species	Access. No.	Mass Spec Data	Mass Database	Mass Difference	AAs	% Coverage	Comments
7	4 peaks match with ribosome L32	mouse	P17832 (Swiss-Pro)	1033.25	1033.17	0.08	67-75	33	
				1098.31	1063.40	-3.03	1-10*		
				1134.72	1134.28	0.44	65-74		
				1449.78	1449.68	0.12	19-29		
	5 peaks match with BMP-3	human	4557371 (NCBI)	1050.42	1060.20	0.22	102-111	21	% coverage calculation is relative to the mature BMP-3, 163 AAS (294-472)
				1113.39	1113.31	0.08	361-363		
				1360.26	1360.58	-0.32	180-200		
				1652.28	1651.91	0.37	410-424		
				1793.62	1794.02	-0.40	346-360		
B	1 peak matches with Lysyl Oxidase RP	human	NP002309 (Swiss-Pro)	2410.37	2410.63	-0.26	645-659	3	12 MS peaks match with Band 4
9	6 peaks match with BMP-3	human	4557371 (NCBI)	1113.14	1113.31	-0.17	361-368	36	% coverage calculation is relative to the mature BMP-3, 163 AAS (294-472)
				1438.60	1438.56	0.02	346-357		
				1566.77	1566.76	0.01	345-357		
				1651.01	1651.01	0.30	410-424		
				2901.67	2901.19	0.48	41-56		
				3400.94	3407.77	1.17	290-318		

Figure 16D Identification of Proteins by Mass Spectrometry of Tryptic Fragments from 1D Gels

Band	Mass Spec Profile	Species	Acc. No.	Mass Spec Data	Mass Database	AAS	% Cover-age	Comments
11	5 peaks match with BMP-3	human	4557371 (NCBI)	1113.23	1113.31	-0.08	361-368	48 % coverage calculation is relative to the mature BMP-3, 1B3 AAS [290-412]
				1651.73	1651.91	-0.18	410-424	
				1795.58	1794.82	-0.44	346-360	
				2424.24	2424.81	-0.57	373-392	
				3408.34	3407.77	0.57	290-318	
	5 peaks match with ribosome L6	human	Q02878 (Swiss-Prof)	1140.36	1140.23	0.15	114-122	16
				1526.88	1526.88	0.02	141-155	
		mouse	P47811 (Swiss-Prof)	1059.15	1059.12	0.03	10-20	
				1145.38	1145.35	0.01	262-271	
				1386.74	1386.68	0.06	260-271	
18	4 peaks match with TGF-β2	human	P08172 (Swiss-Prof)	1101.20	1101.26	-0.06	303-311	52
				1175.26	1175.42	-0.16	400-409	
				2240.37	2240.80	-0.23	312-328	
				2691.70	2691.91	-0.21	340-382	
	5 peaks match with SPP24	bovine	Q27367 (Swiss-Prof)	1410.93	1411.60	-0.67	42-53	30
				1447.59	1447.65	-0.06	113-124	
				1540.84	1540.60	0.04	88-98	
				1868.10	1869.05	0.05	62-77	
				2268.47	2268.57	-0.10	33-53	

Figure 16E Identification of Proteins by Mass Spectrometry of Tryptic Fragments from 1D Gels

Band	Mass Spec Profile	Species	Acc. No.	Mass Spec Data	Mass Spec Database	Mass Difference	AAs	% Coverage	Comments
22	5 peaks match with TGF- β 2	human	P08112 (Swiss- Prot)	1101.15	1101.26	-0.11	303-311	63	
				1175.13	1175.42	0.28	400-409		
				2084.16	2084.42	-0.26	312-347		
				2240.25	2240.60	-0.35	312-328		
				2691.61	2691.91	-0.30	340-362		
	2 peaks match with SPP24	bovine	Q27967 (Swiss- Prot)	1411.23	1411.60	-0.37	42-53	11	
				1447.40	1447.65	-0.25	113-124		
25	5 peaks match with histone H1.x	human	JG4928 (PIR)	1208.46	1208.40	0.06	46-57	14	
				1221.71	1222.35	-0.64	107-118		
				1349.85	1350.52	-0.67	107-119		
				1384.57	1384.59	-0.02	46-58		
				1732.23	1732.97	-0.74	43-57		
	5 peaks match with BMP-3	human	455771 (NCBI)	1060.43	1060.20	0.23	102-111	31	% coverage calculation is relative to the mature BMP- 3, 183 AAS (290-472)
				1438.63	1438.58	0.25	346-357		
				1566.92	1566.76	0.16	345-357		
				1651.80	1651.91	-0.11	410-424		
				3408.86	3407.77	1.09	290-318		

Figure 16F Identification of Proteins by Mass Spectrometry of Tryptic Fragments from 1D Gels

Band	Mass Spec Profile	Species	Acc. No.	Mass Spec Data	Mass Spec Database	Mass Difference	AAS	% Coverage	Comments
29	4 peaks match with BMP-3	human	4557371 (NCB)	1113.22	1113.31	-0.09	361-368	27	% coverage calculation is relative to the mature BMP- 3, 1B3 AAS (29D-472)

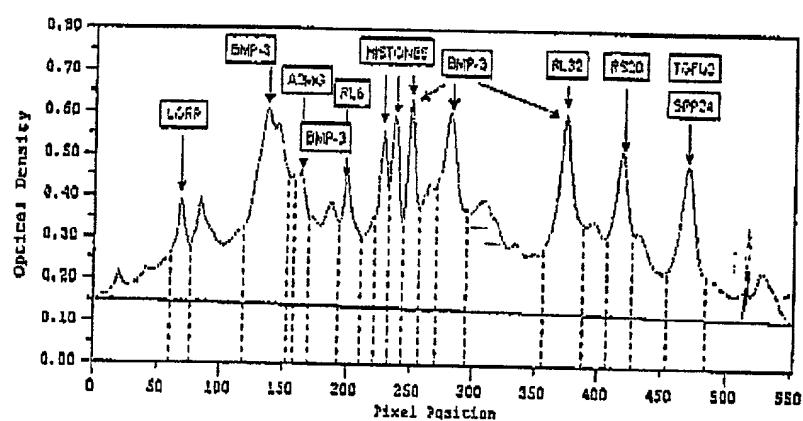


FIGURE 17A

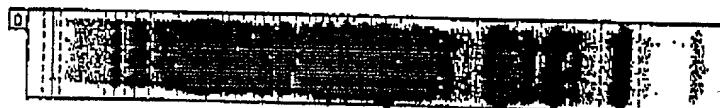


FIGURE 17B

22

Figure 18 Quantitation of Identified BP proteins

Identified Protein	Percentage of Total Protein
LORP	2
BMP-3	11
BMP - 3 & A2-MG	3
RL6 & BMP-3	4
Histone	3
Histone	3
Histone & BMP-3	4
BMP-3	8
RL32 & BMP-3	8
RS20	5
SPP24 & TGF- β 2	6
Total	58%

Figure 124 Identification of Preliminary Mass Spectrometry of Fragments from 2D Gels

Spot	Digest	Mass Spec Profile	Species	Acc. No.	MS Peaks Data	Database	AAs	% Coverage	Comments
1	Lys-C	2 peaks match with Coagulation Factor XIIIa	Human	P05160 (Swiss-Prot)	1837.01	1837.14	-0.13	472-487	
					1921.65	1921.14	0.51	388-382	
					2679.51	N/A	486-504		peptide match confirmed by sequence analysis
2	Trypsin	2 peaks match with LORP	Human	NP002309 (Swiss-Prot)	1609.57	1609.86	-0.31	241-253	
					2410.69	2410.63	0.26	645-659	
3	Lys-C	B peaks match with Cathepsin L Precursor	Bovine	P25975 (Swiss-Prot)	1407.26	1406.80	0.46	105-116	
					1546.84	1546.70	0.14	58-70	
					1831.16	1680.80	0.36	21-33	
					1681.86	1680.80	1.06	301-314	
					1834.71	1834.60	0.71	316-334	
					2352.90	2351.50	1.40	274-285	
					2381.50	2380.70	0.80	239-261	
					2721.51	2721.10	0.41	131-154	

Figure 1C Identification of Proteins by Mass Spectrometry of Fragments from 2D Gels

Figure 1/10 Identification of Proteins by Mass Spectrometry of Fragments from 2D Gels

Spot	Digest	Mass Spec Profile	Species	Acc. No.	MS Peaks	AAS	% Coverage	Comments
					Data Database Diff			
9	Trypsin	7 peaks match S3a	Mouse	P97351 (Swiss-Pro)	920.05 920.10 1218.29 1346.62 1516.69 1593.72 1719.91 1953.12	-0.05 -0.02 -152-161 -1346.49 1516.69 1593.82 1720.00 1953.16	19.26 0.13 151-161 0.13 0.00 0.10 94-106 -0.09 -0.04	29
10	Trypsin	14 peaks match H1.c	Human	876653 (NCBI)	1321.75 1579.70 1707.65 2147.17	0.19 -0.01 -0.24 -0.36	23 65-79 64-79 1-21	
11	Trypsin	6 peaks match S4	Human	P12750 (Swiss-Pro)	1163.48 1216.39 1354.03 1507.81 1557.75 2140.34 2591.80	0.10 1216.39 1353.61 1507.69 1557.98 2140.58 2591.90	230-239 0.00 0.42 0.12 -0.23 -0.24 -0.10	1 23